

OM protein - protein search, using sw model

Run on: April 15, 2004, 13:37:36 ; Search time 50.2 Seconds
(without alignments)
1412.738 Million cell updates/sec

Title: US-08-737-319-1 in PROTEIN DATABASES
Perfect score: 1341
Sequence: 1 MSMPNIVPPAEVRTEGLSLE.....KGEVDAKSLEDLSDNKVWKM 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

PROTEIN SEQ 1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1341	100.0	251	2	AAW00278	wo 96/28545 Aaw00278 Peptide u
2	1341	100.0	251	2	AAW22501	wo 77/23633 Aaw22501 Phaffia d
3	819	61.1	281	7	ADB70021	Adb70021 C. neofor
4	640.5	47.8	271	6	ABJ25766	Abj25766 Aspergill
5	629	46.9	284	5	ABP73637	Abp73637 Candida a
6	627.5	46.8	271	6	ABJ26366	Abj26366 Aspergill
7	579.5	43.2	228	5	ABP62828	Abp62828 Human pol
8	579.5	43.2	228	6	ABU89730	Abu89730 Protein d
9	579.5	43.2	228	7	ADE54597	Ade54597 Human Pro

10	578.5	43.1	288	2	AAW00280	Aaw00280	Peptide u
11	575.5	42.9	288	5	ABG93897	Abg93897	Saccharom
12	560	41.8	227	7	ADE54595	Ade54595	Rat Prote
13	547	40.8	234	3	AAy54297	Aay54297	Amino aci
14	545.5	40.7	295	3	AAy54296	Aay54296	Amino aci
15	541	40.3	238	3	AAy54298	Aay54298	Amino aci
16	539	40.2	238	5	ABG93909	Abg93909	Oryza sat
17	536	40.0	287	5	ABG93895	Abg93895	Clarkia b
18	535.5	39.9	295	5	ABG93907	Abg93907	Adonis pa
19	535	39.9	234	5	ABG93908	Abg93908	Adonis pa
20	532.5	39.7	284	2	AAW35349	Aaw35349	Arabidops
21	532.5	39.7	284	3	AAy54285	Aay54285	An Arabid
22	530.5	39.6	284	3	AAy77972	Aay77972	A. thalia
23	528.5	39.4	225	3	AAG42236	Aag42236	Arabidops
24	528.5	39.4	233	3	AAG42235	Aag42235	Arabidops
25	528.5	39.4	291	3	AAG42234	Aag42234	Arabidops
26	527.5	39.3	280	5	ABG93905	Abg93905	Lactuca s
27	526.5	39.3	229	3	AAy54295	Aay54295	Amino aci
28	526.5	39.3	229	5	ABG93906	Abg93906	Lactuca s
29	525.5	39.2	284	5	ABG93894	Abg93894	Arabipsos
30	523.5	39.0	233	3	AAy54299	Aay54299	Amino aci
31	523.5	39.0	261	2	AAW35348	Aaw35348	Arabidops
32	523.5	39.0	261	3	AAy54286	Aay54286	An Arabid
33	520.5	38.8	261	5	ABG93896	Abg93896	Arabipsos
34	520.5	38.8	280	3	AAy54294	Aay54294	Amino aci
35	517.5	38.6	232	3	AAy54293	Aay54293	Amino aci
36	515.5	38.4	232	5	ABG93904	Abg93904	Tagetes e
37	511.5	38.1	234	4	AAB30549	Aab30549	An isopen
38	511.5	38.1	234	4	AAB99771	Aab99771	Hevea bra
39	510.5	38.1	233	5	ABG93910	Abg93910	Arabipsos
40	510	38.0	232	3	AAy90229	Aay90229	Marigold
41	500	37.3	307	3	AAy54302	Aay54302	Amino aci
42	499	37.2	307	5	ABG93913	Abg93913	Chlamydom
43	494.5	36.9	304	3	AAy54301	Aay54301	Amino aci
44	494	36.8	259	2	AAW00279	Aaw00279	Peptide u
45	493	36.8	305	2	AAW35350	Aaw35350	Haematoco

ALIGNMENTS

RESULT 1

AAW00278

ID AAW00278 standard; protein; 251 AA.

XX

AC AAW00278;

XX

DT 16-OCT-2003 (revised)

DT 14-JAN-1997 (first entry)

XX

DE Peptide used to increase carotenoid yield.

XX

KW Carotenoid; beta-carotene; phytoene; lycopene; zeaxanthin; astaxanthin;

KW Phaffia rhodozyma; Haematococcus pluvialis; Saccharomyces cerevisiae.

XX

OS Xanthophyllomyces dendrorhous.

XX

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OM protein - protein search, using sw model

Run on: April 15, 2004, 13:50:32 ; Search time 13.7804 Seconds
(without alignments)
1752.060 Million cell updates/sec

Title: US-08-737-319-1
Perfect score: 1341
Sequence: 1 MSMPNIVPPAEVRTEGLSLE.....KGEVDAKSLEDLSDNKVWKM 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	616	45.9	227	2	A56442	isopentenyl-diphos
2	579.5	43.2	228	2	A53028	isopentenyl-diphos
3	578.5	43.1	288	2	A34440	isopentenyl-diphos
4	536	40.0	290	2	S49588	isopentenyl-diphos
5	530.5	39.6	233	2	S71369	isopentenyl-diphos
6	530.5	39.6	284	2	S71370	isopentenyl-diphos
7	500	37.3	307	2	T07979	isopentenyl-diphos
8	498	37.1	293	2	T51248	isopentenyl-diphos
9	494	36.8	293	2	T46812	isopentenyl-diphos
10	493	36.8	305	2	T52027	isopentenyl-diphos
11	403.5	30.1	831	2	S44843	K06H7.3 protein -
12	230.5	17.2	219	2	T03399	isopentenyl-diphos
13	209	15.6	197	2	T35275	probable IPP isome

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OM protein - protein search, using sw model

Run on: April 15, 2004, 13:46:31 ; Search time 9.84314 Seconds
(without alignments)
1327.789 Million cell updates/sec

Title: US-08-737-319-1
Perfect score: 1341
Sequence: 1 MSMPNIVPPAEVRTEGLSLE.....KGEVDAKSLEDLSDNKVWKM 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1337	99.7	251	1	IDI1_PHARH	1997 Genbank Q42641 phaffia rho
2	616	45.9	227	1	IDI1_SCHPO	Q10132 schizosacch
3	579.5	43.2	227	1	IDI1_HUMAN	Q13907 homo sapien
4	578.5	43.1	287	1	IDI1_YEAST	P15496 saccharomyc
5	567.5	42.3	227	1	IDI1_MESAU	O35586 mesocricetu
6	562.5	41.9	227	1	IDI1_MOUSE	P58044 mus musculu
7	560	41.8	227	1	IDI1_RAT	O35760 rattus norv
8	536	40.0	287	1	IDI1_CLABR	Q39472 clarkia bre
9	532.5	39.7	235	1	IDI1_CAMAC	O48964 camptotheca
10	530.5	39.6	284	1	IDI2_ARATH	Q42553 arabidopsis
11	528.5	39.4	233	1	IDI1_ARATH	Q38929 arabidopsis
12	520	38.8	309	1	IDI2_CAMAC	O48965 camptotheca
13	507.5	37.8	286	1	IDI2_CLABR	Q39471 clarkia bre
14	506.5	37.8	290	1	IDI2_CLAXA	Q39664 clarkia xan
15	442	33.0	227	1	IDI2_HUMAN	Q9bxs1 homo sapien
16	209	15.6	197	1	IDI_STRCO	Q9x7q6 streptomyce
17	205	15.3	197	1	IDI_STRAW	Q82mj7 streptomyce

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OM protein - protein search, using sw model

Run on: April 15, 2004, 13:47:16 ; Search time 35.4353 Seconds
(without alignments)
2234.921 Million cell updates/sec

Title: US-08-737-319-1
Perfect score: 1341
Sequence: 1 MSMPNIVPPAEVRTEGLSLE.....KGEVDAKSLEDLSDNKNVWKM 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1341	100.0	251	3	Q9UUQ1	Q9uuq1 phaffia rho
2	637	47.5	268	3	Q874I0	Q874i0 emericella
3	636	47.4	234	3	Q8NJL9	Q8njl9 aspergillus
4	579.5	43.2	228	4	Q86U81	Q86u81 homo sapien
5	547.5	40.8	295	10	Q9M6K9	Q9m6k9 adonis pala
6	547	40.8	267	10	Q9M6K8	Q9m6k8 adonis pala
7	541	40.3	238	10	Q8GVZ0	Q8gvz0 oryza sativ
8	541	40.3	254	10	Q9M6K4	Q9m6k4 oryza sativ
9	540	40.3	290	10	Q9AVG8	Q9avg8 nicotiana t
10	532.5	39.7	284	10	Q9M6K3	Q9m6k3 arabidopsis
11	529.5	39.5	235	10	Q9AVG7	Q9avg7 nicotiana t
12	529.5	39.5	263	10	Q9M6K6	Q9m6k6 lactuca sat
13	524	39.1	281	10	Q9M592	Q9m592 brassica ol
14	523.5	39.0	261	10	Q9M6K2	Q9m6k2 arabidopsis
15	522.5	39.0	226	10	Q8S3L7	Q8s3l7 melaleuca a
16	520.5	38.8	280	10	Q9M6K7	Q9m6k7 lactuca sat
17	518.5	38.7	245	10	Q9M6K5	Q9m6k5 tagetes ere
18	518	38.6	224	10	Q9FXR6	Q9fxr6 eucommia ul
19	518	38.6	239	5	Q9NH02	Q9nh02 dictyosteli
20	511.5	38.1	234	10	Q9S7C4	Q9s7c4 hevea brasi
21	510	38.0	262	10	Q9FV48	Q9fv48 tagetes ere
22	507.5	37.8	235	10	Q8S3L8	Q8s3l8 melaleuca a
23	507.5	37.8	235	10	Q84RZ8	Q84rz8 periploca s
24	500	37.3	307	10	081691	081691 chlamydomon
25	498	37.1	293	10	081660	081660 haematococc
26	494	36.8	293	10	Q9SAY0	Q9say0 haematococc
27	493	36.8	305	10	081659	081659 haematococc
28	489	36.5	256	5	Q9VDC2	Q9vdc2 drosophila
29	488	36.4	256	5	Q8MRH1	Q8mrh1 drosophila
30	440	32.8	227	11	Q8BFZ6	Q8bfz6 mus musculu
31	403.5	30.1	236	5	Q9BI81	Q9bi81 caenorhabdi
32	321	23.9	120	10	Q9AVI8	Q9avi8 youngia jap
33	320	23.9	120	10	Q94IE1	Q94iel euphorbia t
34	318	23.7	120	10	Q9AVG5	Q9avg5 sapium sebi
35	313	23.3	120	10	Q9AVJ5	Q9avj5 sonchus ole
36	304	22.7	120	10	Q9AYS6	Q9ays6 sonchus ole
37	301.5	22.5	121	10	Q9AVG6	Q9avg6 taraxacum j
38	301	22.4	119	10	Q9AVJ1	Q9avj1 metaplexis
39	266	19.8	229	5	Q8SSI5	Q8ssi5 encephalito
40	261	19.5	91	10	Q9LLB6	Q9llb6 daucus caro
41	249.5	18.6	197	2	Q8RTW6	Q8rtw6 uncultured
42	230.5	17.2	219	10	P93355	P93355 nicotiana t
43	221.5	16.5	503	16	Q83DT5	Q83dt5 coxiella bu
44	205	15.3	192	2	Q8KZ66	Q8kz66 uncultured
45	181	13.5	172	2	Q8KZ12	Q8kz12 uncultured

ALIGNMENTS

RESULT 1
Q9UUQ1

OM protein - protein search, using sw model

Run on: April 15, 2004, 13:49:12 ; Search time 16.2412 Seconds
(without alignments)
797.856 Million cell updates/sec

Title: US-08-737-319-1
Perfect score: 1341
Sequence: 1 MSMPNIVPPAEVRTEGLSLE.....KGEVDAKSLEDLSDNKVWKM 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1341	100.0	251	4	US-09-091-725-21	Sequence 21, Appl
2	578.5	43.1	288	1	US-08-624-125-19	Sequence 19, Appl
3	578.5	43.1	288	4	US-08-937-155-19	Sequence 19, Appl
4	578.5	43.1	288	4	US-09-323-998E-19	Sequence 19, Appl
5	547	40.8	234	4	US-09-323-998E-40	Sequence 40, Appl
6	545.5	40.7	295	4	US-09-323-998E-39	Sequence 39, Appl
7	541	40.3	238	4	US-09-323-998E-41	Sequence 41, Appl
8	536	40.0	287	1	US-08-624-125-17	Sequence 17, Appl
9	536	40.0	287	4	US-08-937-155-17	Sequence 17, Appl
10	536	40.0	287	4	US-09-323-998E-17	Sequence 17, Appl
11	532.5	39.7	284	1	US-08-624-125-16	Sequence 16, Appl

USPN
6329141

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OM protein - protein search, using sw model

Run on: April 15, 2004, 13:54:22 ; Search time 37.8961 Seconds
(without alignments)
1825.887 Million cell updates/sec

Title: US-08-737-319-1
Perfect score: 1341
Sequence: 1 MSMPNIVPPAEVRTEGLSLE.....KGEVDAKSLEDLSDNKVWKM 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1124875 seqs, 275673149 residues

Total number of hits satisfying chosen parameters: 1124875

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	819	61.1	281	15	US-10-320-797-3065	Sequence 3065, Ap
2	640.5	47.8	271	14	US-10-128-714-3424	Sequence 3424, Ap
3	629	46.9	284	14	US-10-032-585-7474	Sequence 7474, Ap
4	627.5	46.8	271	14	US-10-128-714-8424	Sequence 8424, Ap
5	579.5	43.2	228	12	US-10-363-616-265	Sequence 265, App
6	579.5	43.2	273	15	US-10-369-493-12865	Sequence 12865, A
7	578.5	43.1	288	9	US-09-323-998D-19	Sequence 19, Appl
8	578.5	43.1	288	15	US-10-369-493-22482	Sequence 22482, A
9	574	42.8	267	15	US-10-369-493-2346	Sequence 2346, Ap
10	574	42.8	267	15	US-10-369-493-2351	Sequence 2351, Ap
11	557	41.5	257	15	US-10-369-493-3496	Sequence 3496, Ap
12	547.5	40.8	295	16	US-10-389-566-2294	Sequence 2294, Ap
13	547	40.8	234	9	US-09-323-998D-40	Sequence 40, Appl
14	547	40.8	267	16	US-10-389-566-2295	Sequence 2295, Ap
15	545.5	40.7	295	9	US-09-323-998D-39	Sequence 39, Appl
16	541	40.3	238	9	US-09-323-998D-41	Sequence 41, Appl
17	541	40.3	238	16	US-10-389-566-1985	Sequence 1985, Ap
18	536	40.0	287	9	US-09-323-998D-17	Sequence 17, Appl
19	532.5	39.7	284	9	US-09-323-998D-16	Sequence 16, Appl
20	530.5	39.6	284	14	US-10-342-224-96	Sequence 96, Appl
21	529.5	39.5	263	16	US-10-389-566-2297	Sequence 2297, Ap
22	526.5	39.3	229	9	US-09-323-998D-38	Sequence 38, Appl
23	524	39.1	281	16	US-10-389-566-2306	Sequence 2306, Ap
24	523.5	39.0	233	9	US-09-323-998D-42	Sequence 42, Appl
25	523.5	39.0	261	9	US-09-323-998D-18	Sequence 18, Appl
26	522.5	39.0	226	16	US-10-389-566-1492	Sequence 1492, Ap
27	521	38.9	309	16	US-10-389-566-792	Sequence 792, App
28	520.5	38.8	280	9	US-09-323-998D-37	Sequence 37, Appl
29	520.5	38.8	280	16	US-10-389-566-2296	Sequence 2296, Ap
30	518.5	38.7	245	16	US-10-389-566-2298	Sequence 2298, Ap
31	517.5	38.6	232	9	US-09-323-998D-36	Sequence 36, Appl
32	511.5	38.1	234	16	US-10-389-566-2210	Sequence 2210, Ap
33	510	38.0	262	16	US-10-389-566-2458	Sequence 2458, Ap
34	507.5	37.8	235	16	US-10-389-566-1491	Sequence 1491, Ap
35	506.5	37.8	290	16	US-10-389-566-2247	Sequence 2247, Ap
36	500	37.3	307	9	US-09-323-998D-45	Sequence 45, Appl
37	498	37.1	293	16	US-10-389-566-2102	Sequence 2102, Ap
38	494	36.8	293	16	US-10-389-566-2125	Sequence 2125, Ap
39	493	36.8	305	9	US-09-323-998D-14	Sequence 14, Appl
40	493	36.8	305	9	US-09-323-998D-44	Sequence 44, Appl
41	493	36.8	305	16	US-10-389-566-2101	Sequence 2101, Ap
42	490	36.5	194	9	US-09-925-302-585	Sequence 585, App
43	490	36.5	194	12	US-09-925-302-585	Sequence 585, App
44	490	36.5	293	9	US-09-323-998D-15	Sequence 15, Appl
45	490	36.5	293	9	US-09-323-998D-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-10-320-797-3065

OM protein - protein search, using sw model

Run on: April 15, 2004, 13:37:36 ; Search time 51.8 Seconds
(without alignments)
1412.738 Million cell updates/sec

Title: US-08-737-319-2 in PRT databases
Perfect score: 1398
Sequence: 1 MQLLAEDRTDHMRGASTWAG.....AALNTDKHEDWGTVHHINEA 259

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Seq 2 in protein databases

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match	Length				
1	1398	100.0	259	2	AAW00279	WO 96/28545	Aaw00279 Peptide u
2	1383	98.9	293	2	AAW35351	WO 97/36998	Aaw35351 Haematoco
3	1383	98.9	293	3	AAAY54300	WO 99/63055	Aay54300 Amino aci
4	1383	98.9	293	3	AAAY54288		Aay54288 An isopen
5	1372	98.1	293	5	ABG93893	USPAP 2002/02631	Abg93893 H. pluvia
6	1372	98.1	293	5	ABG93911		Abg93911 Haematoco
7	1368	97.9	305	2	AAW35350		Aaw35350 Haematoco
8	1368	97.9	305	3	AAAY54287		Aay54287 An isopen
9	1360	97.3	305	5	ABG93892		Abg93892 H. pluvia
10	1352.5	96.7	304	3	AAAY54301		Aay54301 Amino aci
11	1345.5	96.2	304	5	ABG93912		Abg93912 Haematoco
12	777.5	55.6	307	3	AAAY54302		Aay54302 Amino aci
13	775.5	55.5	307	5	ABG93913		Abg93913 Chlamydom

Anal. earliest 03/1996
earliest 06/1998

OM protein - protein search, using sw model

Run on: April 15, 2004, 13:50:32 ; Search time 14.2196 Seconds
(without alignments)
1752.060 Million cell updates/sec

Title: US-08-737-319-2
Perfect score: 1398
Sequence: 1 MQLLAEDRTDHMRGASTWAG.....AALNTDKHEDWGTVHHINEA 259

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID		Description
		Match	Length				
1	1398	100.0	293	2	T46812	03/2000	isopentenyl-diphos
2	1394	99.7	293	2	T51248	07/2000	isopentenyl-diphos
3	1368	97.9	305	2	T52027	10/2000	isopentenyl-diphos
4	777.5	55.6	307	2	T07979		isopentenyl-diphos
5	530	37.9	290	2	S49588		isopentenyl-diphos
6	523	37.4	233	2	S71369		isopentenyl-diphos
7	522	37.3	227	2	A56442		isopentenyl-diphos
8	515	36.8	284	2	S71370		isopentenyl-diphos
9	496	35.5	288	2	A34440		isopentenyl-diphos
10	495.5	35.4	228	2	A53028		isopentenyl-diphos
11	398	28.5	831	2	S44843		K06H7.3 protein -
12	264	18.9	219	2	T03399		isopentenyl-diphos
13	255.5	18.3	197	2	T35275		probable IPP isome

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OM protein - protein search, using sw model

Run on: April 15, 2004, 13:46:31 ; Search time 10.1569 Seconds
(without alignments)
1327.789 Million cell updates/sec

Title: US-08-737-319-2
Perfect score: 1398
Sequence: 1 MQLLAEDRTDHMRGASTWAG.....AALNTDKHEDWGTVHHINEA 259

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	533	38.1	235	1	IDI1_CAMAC	Q48964 camptotheca
2	530	37.9	287	1	IDI1_CLABR	Q39472 clarkia bre
3	526.5	37.7	309	1	IDI2_CAMAC	Q48965 camptotheca
4	526	37.6	233	1	IDI1_ARATH	Q38929 arabidopsis
5	524.5	37.5	286	1	IDI2_CLABR	Q39471 clarkia bre
6	522	37.3	227	1	IDI1_SCHPO	Q10132 schizosacch
7	515	36.8	284	1	IDI2_ARATH	Q42553 arabidopsis
8	515	36.8	290	1	IDI2_CLAXA	Q39664 clarkia xan
9	496	35.5	287	1	IDI1_YEAST	P15496 saccharomyc
10	493.5	35.3	227	1	IDI1_HUMAN	Q13907 homo sapien
11	491	35.1	251	1	IDI1_PHARH	Q42641 phaffia rho
12	473	33.8	227	1	IDI1_MOUSE	P58044 mus musculu
13	472	33.8	227	1	IDI1_RAT	Q35760 rattus norv
14	471.5	33.7	227	1	IDI1_MESAU	Q35586 mesocricetu
15	415	29.7	227	1	IDI2_HUMAN	Q9bxs1 homo sapien
16	266	19.0	197	1	IDI_STRAW	Q82mj7 streptomyce
17	255.5	18.3	197	1	IDI_STRCO	Q9x7q6 streptomyce

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OM protein - protein search, using sw model

Run on: April 15, 2004, 13:47:16 ; Search time 36.5647 Seconds
(without alignments)
2234.921 Million cell updates/sec

Title: US-08-737-319-2
Perfect score: 1398
Sequence: 1 MQLLAEDRTDHMRGASTWAG.....AALNTDKHEDWGTVHHINEA 259

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1398	100.0	293	10	Q9SAY0	Q9say0 haematococc
2	1394	99.7	293	10	081660	081660 haematococc
3	1368	97.9	305	10	081659	081659 haematococc
4	777.5	55.6	307	10	081691	081691 chlamydomon
5	538	38.5	234	3	Q8NJL9	Q8njl9 aspergillus
6	534	38.2	268	3	Q874I0	Q874i0 emericella
7	530.5	37.9	226	10	Q8S3L7	Q8s3l7 melaleuca a
8	527	37.7	238	10	Q8GVZ0	Q8gvz0 oryza sativ
9	527	37.7	254	10	Q9M6K4	Q9m6k4 oryza sativ
10	527	37.7	263	10	Q9M6K6	Q9m6k6 lactuca sat
11	524	37.5	235	10	Q9AVG7	Q9avg7 nicotiana t
12	523	37.4	262	10	Q9FV48	Q9fv48 tagetes ere
13	522	37.3	245	10	Q9M6K5	Q9m6k5 tagetes ere
14	522	37.3	284	10	Q9M6K3	Q9m6k3 arabidopsis
15	521	37.3	261	10	Q9M6K2	Q9m6k2 arabidopsis
16	520	37.2	224	10	Q9FXR6	Q9fxr6 eucommia ul
17	519.5	37.2	235	10	Q8S3L8	Q8s3l8 melaleuca a
18	517	37.0	234	10	Q9S7C4	Q9s7c4 hevea brasi
19	517	37.0	267	10	Q9M6K8	Q9m6k8 adonis pala
20	517	37.0	290	10	Q9AVG8	Q9avg8 nicotiana t
21	516	36.9	280	10	Q9M6K7	Q9m6k7 lactuca sat
22	510	36.5	295	10	Q9M6K9	Q9m6k9 adonis pala
23	509	36.4	235	10	Q84RZ8	Q84rz8 periploca s
24	509	36.4	281	10	Q9M592	Q9m592 brassica ol
25	501	35.8	256	5	Q9VDC2	Q9vdc2 drosophila
26	500	35.8	256	5	Q8MRH1	Q8mrh1 drosophila
27	495.5	35.4	228	4	Q86U81	Q86u81 homo sapien
28	494	35.3	251	3	Q9UUQ1	Q9uuq1 phaffia rho
29	455.5	32.6	239	5	Q9NH02	Q9nh02 dictyosteli
30	398	28.5	236	5	Q9BI81	Q9bi81 caenorhabdi
31	379	27.1	227	11	Q8BFZ6	Q8bfz6 mus musculu
32	283	20.2	120	10	Q9AVI8	Q9avi8 youngia jap
33	276	19.7	120	10	Q9AYS6	Q9ays6 sonchus ole
34	275	19.7	120	10	Q94IE1	Q94iel1 euphorbia t
35	273	19.5	120	10	Q9AVJ5	Q9avj5 sonchus ole
36	272	19.5	229	5	Q8SSI5	Q8ssi5 encephalito
37	267	19.1	120	10	Q9AVG5	Q9avg5 sapium sebi
38	264	18.9	219	10	P93355	P93355 nicotiana t
39	256.5	18.3	121	10	Q9AVG6	Q9avg6 taraxacum j
40	243.5	17.4	119	10	Q9AVJ1	Q9avj1 metaplexis
41	236.5	16.9	197	2	Q8RTW6	Q8rtw6 uncultured
42	225.5	16.1	91	10	Q9LLB6	Q9llb6 daucus caro
43	225	16.1	192	2	Q8KZ66	Q8kz66 uncultured
44	204.5	14.6	503	16	Q83DT5	Q83dt5 coxiella bu
45	192	13.7	172	2	Q8KZ12	Q8kz12 uncultured

ALIGNMENTS

RESULT 1
Q9SAY0

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OM protein - protein search, using sw model

Run on: April 15, 2004, 13:49:12 ; Search time 16.7588 Seconds
(without alignments)
797.856 Million cell updates/sec

Title: US-08-737-319-2
Perfect score: 1398
Sequence: 1 MQLLAEDRTDHMRGASTWAG.....AALNTDKHEDWGTVHHINEA 259

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						Description
Result No.	Score	% Query Match	Length	DB	ID	
1	1383	98.9	293	1	US-08-624-125-15	5744341 Sequence 15, Appl
2	1383	98.9	293	4	US-08-937-155-15	6524811 Sequence 15, Appl
3	1383	98.9	293	4	US-09-323-998E-15	6642021 Sequence 15, Appl
4	1383	98.9	293	4	US-09-323-998E-43	" Sequence 43, Appl
5	1368	97.9	305	1	US-08-624-125-14	Sequence 14, Appl
6	1368	97.9	305	4	US-08-937-155-14	Sequence 14, Appl
7	1368	97.9	305	4	US-09-323-998E-14	Sequence 14, Appl
8	1368	97.9	305	4	US-09-323-998E-44	Sequence 44, Appl
9	777.5	55.6	307	4	US-09-323-998E-45	Sequence 45, Appl
10	530	37.9	287	1	US-08-624-125-17	Sequence 17, Appl
11	530	37.9	287	4	US-08-937-155-17	Sequence 17, Appl

Cunningham family

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OM protein - protein search, using sw model

Run on: April 15, 2004, 13:54:22 ; Search time 39.1039 Seconds
(without alignments)
1825.887 Million cell updates/sec

Title: US-08-737-319-2
Perfect score: 1398
Sequence: 1 MQLLAEDRTDHMRGASTWAG.....AALNTDKHEDWGTVHHINEA 259

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1124875 seqs, 275673149 residues

Total number of hits satisfying chosen parameters: 1124875

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

USPAP 2004
0025202
earliest 6/2002

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1398	100.0	293	16	US-10-389-566-2125	Sequence 2125, Ap
2	1394	99.7	293	16	US-10-389-566-2102	Sequence 2102, Ap
3	1383	98.9	293	9	US-09-323-998D-15	Sequence 15, Appl
4	1383	98.9	293	9	US-09-323-998D-43	Sequence 43, Appl
5	1368	97.9	305	9	US-09-323-998D-14	Sequence 14, Appl
6	1368	97.9	305	9	US-09-323-998D-44	Sequence 44, Appl
7	1368	97.9	305	16	US-10-389-566-2101	Sequence 2101, Ap
8	777.5	55.6	307	9	US-09-323-998D-45	Sequence 45, Appl
9	538	38.5	271	14	US-10-128-714-3424	Sequence 3424, Ap
10	530.5	37.9	226	16	US-10-389-566-1492	Sequence 1492, Ap
11	530	37.9	287	9	US-09-323-998D-17	Sequence 17, Appl
12	527	37.7	229	9	US-09-323-998D-38	Sequence 38, Appl
13	527	37.7	238	9	US-09-323-998D-41	Sequence 41, Appl
14	527	37.7	238	16	US-10-389-566-1985	Sequence 1985, Ap
15	527	37.7	263	16	US-10-389-566-2297	Sequence 2297, Ap
16	526	37.6	271	14	US-10-128-714-8424	Sequence 8424, Ap
17	523	37.4	262	16	US-10-389-566-2458	Sequence 2458, Ap
18	522	37.3	245	16	US-10-389-566-2298	Sequence 2298, Ap
19	522	37.3	284	9	US-09-323-998D-16	Sequence 16, Appl
20	521	37.3	233	9	US-09-323-998D-42	Sequence 42, Appl
21	521	37.3	261	9	US-09-323-998D-18	Sequence 18, Appl
22	519.5	37.2	235	16	US-10-389-566-1491	Sequence 1491, Ap
23	518	37.1	232	9	US-09-323-998D-36	Sequence 36, Appl
24	517	37.0	234	9	US-09-323-998D-40	Sequence 40, Appl
25	517	37.0	234	16	US-10-389-566-2210	Sequence 2210, Ap
26	517	37.0	267	16	US-10-389-566-2295	Sequence 2295, Ap
27	516	36.9	280	9	US-09-323-998D-37	Sequence 37, Appl
28	516	36.9	280	16	US-10-389-566-2296	Sequence 2296, Ap
29	515	36.8	284	14	US-10-342-224-96	Sequence 96, Appl
30	515	36.8	290	16	US-10-389-566-2247	Sequence 2247, Ap
31	513	36.7	284	14	US-10-032-585-7474	Sequence 7474, Ap
32	510	36.5	295	16	US-10-389-566-2294	Sequence 2294, Ap
33	510	36.5	309	16	US-10-389-566-792	Sequence 792, App
34	509	36.4	281	16	US-10-389-566-2306	Sequence 2306, Ap
35	504	36.1	295	9	US-09-323-998D-39	Sequence 39, Appl
36	496	35.5	288	9	US-09-323-998D-19	Sequence 19, Appl
37	496	35.5	288	15	US-10-369-493-22482	Sequence 22482, A
38	495.5	35.4	228	12	US-10-363-616-265	Sequence 265, App
39	488	34.9	281	15	US-10-320-797-3065	Sequence 3065, Ap
40	487	34.8	267	15	US-10-369-493-2346	Sequence 2346, Ap
41	487	34.8	267	15	US-10-369-493-2351	Sequence 2351, Ap
42	477	34.1	273	15	US-10-369-493-12865	Sequence 12865, A
43	476.5	34.1	257	15	US-10-369-493-3496	Sequence 3496, Ap
44	448	32.0	259	16	US-10-389-566-925	Sequence 925, App
45	445.5	31.9	194	9	US-09-925-302-585	Sequence 585, App

ALIGNMENTS

RESULT 1
US-10-389-566-2125